

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 091992,840  
Source: TFW16  
Date Processed by STIC: 1/22/07

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/22/2007

PATENT APPLICATION: US/09/992,840

TIME: 13:15:04

Input Set : A:\Cura 57A Seq List.txt

Output Set: N:\CRF4\01222007\I992840.raw

```

3 <110> APPLICANT: Boldog, Ferenc L.;
4   Burgess, Catherine E.;
5   Fernandes, Elma ;
6   Ioime, Noelle ;
7   Jeffers, Michael E.;
8   LaRochelle, William J.;
9   Lichenstein, Henri ;
10  Prayaga, Sudhirdas ;
11  Rittman, Beth ;
12  Shimkets, Richard A.;
13  Shimkets, Juliette B;
14  Yang, Meijia
16 <120> TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease Using Growth Factors
18 <130> FILE REFERENCE: 15966-557A (Cura 57A)
20 <140> CURRENT APPLICATION NUMBER: 09/992840
21 <141> CURRENT FILING DATE: 2001-11-06
23 <150> PRIOR APPLICATION NUMBER: 60/246206
24 <151> PRIOR FILING DATE: 2000-11-06
26 <160> NUMBER OF SEQ ID NOS: 28
28 <170> SOFTWARE: CuraSeqList ver. 0.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 633
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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38 gtgggttcgc atttcctggt gcctcctgcc ggggagcggc cgccgctgct gggcgagcgc 120
40 aggagcgcgg cggagcggag cgcgcgcggc gggccggggg ctgcgcagct ggcgcacctg 180
42 cacggcatcc tgcgcgcggc gcagctctat tgccgcaccg gcttccacct gcagatcctg 240
44 cccgacggca gcgtgcaggg caccgcggcag gaccacagcc tcttcggtat cttggaattc 300
46 atcagtgtgg cagtgggact ggtcagtatt agaggtgtgg acagtggctc ctatctttagg 360
48 atgaatgaca aaggagaact ctatggatca gagaaactta cttccgaatg catctttagg 420
50 gagcagtttg aagagaactg gtataacacc tattcatcta acatatataa acatggagac 480
52 actggccgca ggtattttgt ggcacttaac aaagacggaa ctccaagaga tggcgccagg 540
54 tccaagaggc atcagaaatt tacacatttc ttacctagac cagtggatcc agaaagagtt 600
56 ccagaattgt acaaggacct actgatgtac act 633
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 211
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
65 Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly
66 1 5 10 15

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68 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
69          20          25          30
71 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
72          35          40          45
74 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
75          50          55          60
77 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
78 65          70          75          80
80 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
81          85          90          95
83 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
84          100          105          110
86 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
87          115          120          125
89 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
90          130          135          140
92 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
93 145          150          155          160
95 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
96          165          170          175
98 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
99          180          185          190
101 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
102          195          200          205
104 Met Tyr Thr
105          210
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 1828
109 <212> TYPE: DNA
110 <213> ORGANISM: Homo sapiens
112 <400> SEQUENCE: 3
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115 atttcttctg tcagaaatac ataaaacttt attatatcag cgcagggcgg cgcggcgctg 120
117 gtcccgaggag cagaaccggg ctttttcttg gagcgacgct gtctctagtc gctgatccca 180
119 aatgcaccgg ctcatctttg tctacactct aatctgcgca aacttttgca gctgtcggga 240
121 cacttctgca accccgcaga ggcacatccat caaagctttg cgcaacgcca acctcaggcg 300
123 agatgagagc aatcacctca cagacttgta ccgaagagat gagaccatcc aggtgaaagg 360
125 aaacggctac gtgcagagtc ctagattccc gaacagctac cccaggaacc tgctcctgac 420
127 atggcggtct cactctcagg agaatacacg gatacagcta gtgtttgaca atcagtttgg 480
129 attagaggaa gcagaaaatg atatctgtag gtatgatttt gtggaagttg aagatatatc 540
131 cgaaaccagt accattatta gaggacgatg gtgtggacac aaggaagttc ctccaaggat 600
133 aaaatcaaga acgaaccaaa ttaaaatcac attcaagtcc gatgactact ttgtggctaa 660
135 acctggattc aagatttatt attctttgct ggaagatttc caaccgcgag cagcttcaga 720
137 gaccaactgg gaatctgtca caagctctat ttcaggggta tcctataact ctccatcagt 780
139 aacggatccc actctgattg cggatgctct ggacaaaaaa attgcagaat ttgatacagt 840
141 ggaagatctg ctcaagtact tcaatccaga gtcattggca gaagatcttg agaatatgta 900
143 tctggacacc cctcggtatc gaggcaggtc ataccatgac cggaagtcaa aagttgacct 960
145 ggataggctc aatgatgatg ccaagcggtta cagttgcact cccaggaatt actcggtcaa 1020
147 tataagagaa gagctgaagt tggccaatgt ggtcttcttt ccacgttgcc tctcgtgca 1080

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```

149 gcgctgtgga ggaaattgtg gctgtggaac tgtcaactgg aggtcctgca catgcaattc 1140
151 agggaaaacc gtgaaaaagt atcatgaggt attacagttt gagcctggcc acatcaagag 1200
153 gaggggtaga gctaagacca tggctctagt tgacatccag ttggatcacc atgaacgatg 1260
155 tgattgtatc tgcagctcaa gaccacctcg ataagagaat gtgcacatcc ttacattaag 1320
157 cctgaaagaa ccttttagttt aaggagggtg agataagaga cctttttcct accagcaacc 1380
159 aaacttacta ctagcctgca atgcaatgaa cacaagtggg tgctgagtct cagccttgct 1440
161 ttgttaatgc catggcaagt agaaaggtat atcatcaact tctataccta agaatatagg 1500
163 attgcattta ataatagtgt ttgagggttat atatgcacaa acacacacag aaatatattc 1560
165 atgtctatgt gtatatagat caaatgtttt ttttggtata tataaccagg tacaccagag 1620
167 cttacatatg tttgagttag actcttaaaa tcctttgcca aaataaggga tgggtcaaata 1680
169 tatgaaacat gtcttttagaa aatttaggag ataaatttat ttttaaattt tgaaacacaa 1740
171 aacaattttg aatcttgctc tcttaaagaa agcatcttgt atattaaaaa tcaaaagatg 1800
173 aggctttctt acatatacat cttagttg                                     1828

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175 &lt;210&gt; SEQ ID NO: 4

176 &lt;211&gt; LENGTH: 370

177 &lt;212&gt; TYPE: PRT

178 &lt;213&gt; ORGANISM: Homo sapiens

180 &lt;400&gt; SEQUENCE: 4

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181 Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
182 1 5 10 15
184 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
185 20 25 30
187 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
188 35 40 45
190 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
191 50 55 60
193 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
194 65 70 75 80
196 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
197 85 90 95
199 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
200 100 105 110
202 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
203 115 120 125
205 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
206 130 135 140
208 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
209 145 150 155 160
211 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
212 165 170 175
214 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
215 180 185 190
217 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
218 195 200 205
220 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
221 210 215 220
223 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
224 225 230 235 240
226 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser

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227          245          250          255
229 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
230          260          265          270
232 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
233          275          280          285
235 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
236          290          295          300
238 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
239 305          310          315          320
241 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
242          325          330          335
244 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
245          340          345          350
247 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
248          355          360          365
250 Pro Arg
251          370
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 1587
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo sapiens
258 <400> SEQUENCE: 5
259 agaggctctc aaattagatc aagaaatgcc tttaacagaa gtgaagagtg aacctgctcc 60
261 tgacatggcg gcttcactct caggagaata cacggataca gctagtgttt gacaatcagt 120
263 ttggattaga ggaagcagaa aatgatatct gtaggtatga ttttgtggaa gttgaagata 180
265 tatccgaaac cagtaccatt attagaggac gatggtgtgg acacaaggaa gtctctccaa 240
267 ggataaaatc aagaacgaac caaattaaaa tcacattcaa gtccgatgac tactttgtgg 300
269 ctaaacctgg attcaagatt tattattctt tgctggaaga tttccaaccc gcagcagctt 360
271 cagagaccaa ctgggaatct gtcacaagct ctatttcagg ggtatcctat aactctccat 420
273 cagtaacgga tcccactctg attgcggatg ctctggacaa aaaaattgca gaatttgata 480
275 cagtggaaga tctgctcaag tacttcaatc cagagtcatg gcaagaagat cttgagaata 540
277 tgtatctgga caccctcggg tatcgaggca ggtcatacca tgaccggaag tcaaaagttg 600
279 acctggatag gctcaatgat gatgccaagc gttacagttg cactcccagg aattactcgg 660
281 tcaatataag agaagagctg aagttggcca atgtggtctt ctttccacgt tgcctcctcg 720
283 tgcagcgtcg tggaggaaat tgtggctgtg gaactgtcaa ctggaggtcc tgcacatgca 780
285 attcagggaa aaccgtgaaa aagtatcatg aggtattaca gtttgagcct ggccacatca 840
287 agaggagggg tagagctaag accatggctc tagttgacat ccagttggat caccatgaac 900
289 gatgtgattg tatctgcagc tcaagaccac ctcgataaga gaatgtgcac atccttacat 960
291 taagcctgaa agaaccttta gtttaaggag ggtgagataa gagacccttt tcctaccagc 1020
293 aaccaaactt actactagcc tgcaatgcaa tgaacacaag tggttgctga gtctcagcct 1080
295 tgctttgtta atgccatggc aagtagaaag gtatatcatc aacttctata cctaagaata 1140
297 taggattgca ttaataata gtgtttgagg ttatatatgc acaaacacac acagaaatat 1200
299 attcatgtct atgtgtatat agatcaaatag ttttttttgg tatatataac cagggtacacc 1260
301 agagcttaca tatgtttgag ttagactctt aaaatccttt gccaaaataa gggatgggtca 1320
303 aatatatgaa acatgtcttt agaaaattta ggagataaat ttatttttaa attttgaaac 1380
305 acaaaacaat tttgaatctt gctctcttaa agaaagcatc ttgtatatta aaaatcaaaa 1440
307 gatgaggctt tcttacatat acatcttagt tgattattaa aaaaggaaaa atatggtttc 1500
309 cagagaaaag gccaatacct aagcattttt tccatgagaa gcactgcata cttacctatg 1560
311 tggactataa taacctgtct ccaaaac 1587

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313 <210> SEQ ID NO: 6
314 <211> LENGTH: 132
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 6
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322 Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr
323           20           25           30
325 Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys
326           35           40           45
328 Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys
329           50           55           60
331 Gly Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys
332           65           70           75           80
334 Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu
335           85           90           95
337 Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val
338           100           105           110
340 Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser
341           115           120           125
343 Arg Pro Pro Arg
344           130
346 <210> SEQ ID NO: 7
347 <211> LENGTH: 1113
348 <212> TYPE: DNA
349 <213> ORGANISM: Homo sapiens
351 <400> SEQUENCE: 7
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354 actttttgcga ctccgcagag agcatccatc aaagctttgc gcaatgccaa cctcaggaga 120
356 gatgagagca atcacctcac agacttgtag cagagagagg agaacattca ggtgacaagc 180
358 aatggccatg tgcagagtcc tcgcttcccc aacagctacc caaggaacct gcttctgaca 240
360 tgggtggctcc gttcccagga gaaaacacgg atacaactgt cctttgacca tcaattcgga 300
362 ctagaggaag cagaaaatga catttgtagg tatgactttg tgggaagttga agaagtctca 360
364 gagagcagca ctgttgtcag aggaagatgg tgtggccaca aggagatccc tccaaggata 420
366 acgtcaagaa caaaccagat taaaatcaca tttaagtctg atgactactt tgtggcaaaa 480
368 cctggattca agatttatta ttcatTTgtg gaagatttcc aaccggaagc agcctcagag 540
370 accaactggg aatcagtcac aagctctttc tctgggggtg cctatcactc tccatcaata 600
372 acggacccca ctctcactgc tgatgccctg gacaaaactg tcgcagaatt cgataccgtg 660
374 gaagatctac ttaagcactt caatccagtg tcttggcaag atgatctgga gaatttgtat 720
376 ctggacaccc ctcatatatag aggcaggtca taccatgatc ggaagtcaa agtggacctg 780
378 gacaggctca atgatgatgt caagcgttac agttgcactc ccaggaatca ctctgtgaac 840
380 ctcagggagg agctgaagct gaccaatgca gtcttcttcc cacgatgcct cctcgtgcag 900
382 cgctgtggtg gcaactgtgg ttgcggaact gtcaactgga agtcctgcac atgcagctca 960
384 ggggaagacag tgaagaagta tcatgaggta ttgaagtttg agcctggaca tttcaagaga 1020
386 aggggcaaaag ctaagaatat ggctcttggt gatatccagc tggatcatca tgagcgatgt 1080
388 gactgtatct gcagctcaag accacctcga taa 1113
390 <210> SEQ ID NO: 8
391 <211> LENGTH: 370

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**VERIFICATION SUMMARY**

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